

SEQUENCE LISTING

RECEIVED THE

TECH CENTER 1600/2800

<110>	Panacci	io,	Michael
	Hasse,	Det	lef

nasse, Detter											
<120> THERAPEUTIC AND DIAGNOSTIC COMPOSITIONS											
<130> DAVIE60.001APC											
<140> 09/077574 <141> 1998-09-24											
<160> 34											
<170> FastSEQ for Windows Version 4.0											
<210> 1 <211> 1647 <212> DNA <213> Lawsonia intracellularis											
<220> <221> CDS <222> (1)(1644)											
<pre><400> 1 atg gct tct aaa gaa atc ctt ttt gat gct aaa gcc cgt gaa aaa ctt</pre>											
tca cga ggt gta gat aaa ctt gca aat gct gtt aaa gta aca ctt gga 96 Ser Arg Gly Val Asp Lys Leu Ala Asn Ala Val Lys Val Thr Leu Gly 20 25 30											
cct aaa ggc cgt aat gtc gtt att gaa aag tct ttt ggt tcc cca gtt 14 Pro Lys Gly Arg Asn Val Val Ile Glu Lys Ser Phe Gly Ser Pro Val 35 40 45	4										
att aca aaa gat ggt gta tct gtt gca aaa gaa att gaa ctt gaa gat Ile Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Glu Asp 50 55 60	2										
aag ttt gaa aat atg ggc gct caa atg gtt aaa gaa gta gct ccc aaa 24 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Pro Lys 65 70 75 80	0										
act agc gat att gct ggt gat gga act aca aca gca aca gtc ctt gca Thr Ser Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala 85 90 95	8										
caa gct att tat cgt gaa ggt gta aaa ctt gta gca gct ggt cgt aat 33 Gln Ala Ile Tyr Arg Glu Gly Val Lys Leu Val Ala Ala Gly Arg Asn 100 105 110	6										
cct atg gcc att aaa cgt ggc ata gat aaa gct gtt gtt gct gtt act 38	4										

Pro	Met	Ala 115	Ile	Lys	Arg	Gly	Ile 120	Asp	Lys	Ala	Val	Val 125	Ala	Val	Thr				
					att Ile										ata Ile	432			
					att Ile 150											480			
					atg Met											528			
					ggt Gly											576			
					ggc Gly											624			
					gaa Glu											672			
					atg Met 230											720			
					cca Pro											768			
-	-		-		ctt Leu	_	_		_		_		_			816			
					gct Ala											864			
					atc Ile											912	·		
					gaa Glu 310											960			
					gac Asp											1008			
					att Ile											1056			
										2									

340		345	350	
	_	gat cgt gaa aaa c Asp Arg Glu Lys I		1104
		gct gtt atc cat g Ala Val Ile His V 380		1152
		aag gat cgt gta g Lys Asp Arg Val G 395		1200
		gaa ggt att gtc c Glu Gly Ile Val F 410		1248
		gtc ctt gat gat a Val Leu Asp Asp I 425		1296
		aat atc atc cgt c Asn Ile Ile Arg A	_	1344
		aat gct ggc tat g Asn Ala Gly Tyr 6 460		1392
		aaa gat ggt ttt g Lys Asp Gly Phe G 475		1440
		att aaa gct ggt g Ile Lys Ala Gly V 490		1488
		caa aat gca gca t Gln Asn Ala Ala S 505		1536
		att gct gaa aaa c Ile Ala Glu Lys F 5		1584
		ggt atg ggt ggt a Gly Met Gly Gly M 540		1632
gac ggt atg tac Asp Gly Met Tyr 545	tag			1647

<210> 2 <211> 548 <212> PRT <213> Lawsonia intracellularis <400> 2

Met Ala Ser Lys Glu Ile Leu Phe Asp Ala Lys Ala Arq Glu Lys Leu Ser Arg Gly Val Asp Lys Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Lys Gly Arg Asn Val Val Ile Glu Lys Ser Phe Gly Ser Pro Val 40 Ile Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Glu Asp 55 60 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Pro Lys 70 75 Thr Ser Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala 90 Gln Ala Ile Tyr Arg Glu Gly Val Lys Leu Val Ala Ala Gly Arg Asn 100 105 Pro Met Ala Ile Lys Arg Gly Ile Asp Lys Ala Val Val Ala Val Thr 120 Lys Glu Leu Ser Asp Ile Thr Lys Pro Thr Arg Asp Gln Lys Glu Ile 135 140 Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Thr Thr Ile Gly Asn 150 155 Ile Ile Ala Glu Ala Met Ala Lys Val Gly Lys Gly Gly Val Ile Thr 165 170 Val Glu Glu Ala Lys Gly Leu Glu Thr Thr Leu Asp Val Val Glu Gly 185 Met Lys Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Pro 200 Glu Lys Met Val Cys Glu Leu Asp Asn Pro Tyr Ile Leu Cys Asn Glu 220 215 Lys Lys Ile Thr Ser Met Lys Asp Met Leu Pro Ile Leu Glu Gln Val 230 235 Ala Lys Val Asn Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly 250 245 Glu Ala Leu Ala Thr Leu Val Val Asn Lys Leu Arg Gly Ala Leu Gln 265 Val Val Ala Val Lys Ala Pro Gly Phe Gly Glu Arg Arg Lys Ala Met 280 285 Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Glu Ala Ile Phe Glu Asp 295 300 Arg Gly Ile Lys Leu Glu Asn Val Ser Leu Ser Ser Leu Gly Thr Ala 310 315 Lys Arg Val Val Ile Asp Lys Glu Asn Thr Thr Ile Val Asp Gly Ala 330 Gly Lys Ser Glu Asp Ile Lys Ala Arg Val Lys Gln Ile Arg Ala Gln 340 345 Ile Glu Glu Thr Ser Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg 360 Leu Ala Lys Leu Val Gly Gly Val Ala Val Ile His Val Gly Ala Ala 375 380 Thr Glu Thr Glu Met Lys Glu Lys Lys Asp Arg Val Glu Asp Ala Leu 390 395 Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly 405 410 Thr Ala Phe Val Arg Ser Ile Lys Val Leu Asp Asp Ile Lys Pro Ala

Asp Asp Asp Glu Leu Ala Gly Leu Asn Tle Ile Arg Arg Ser Leu Glu 435 Glu Pro Leu Arg Gln Ile Ala Ala Asn Ala Gly Tyr Glu Gly Ser Ile 450 Val Val Glu Lys Val Arg Glu Pro Lys Asp Gly Phe Gly Phe Asn Ala 465 470 Ala Ser Gly Glu Tyr Glu Asp Leu Ile Lys Ala Gly Val Ile Asp Pro 485 490 495 Lys Lys Val Thr Arg Ile Ala Leu Gln Asn Ala Ala Ser Val Ala Ser 500 Leu Leu Thr Thr Glu Cys Ala Ile Ala Glu Lys Pro Glu Pro Lys 515 520 Leu Leu Cheu Thr Glu Cys Ala Ile Ala Glu Lys Pro Glu Pro Lys 515 520 Leu Leu Thr Thr Glu Cys Ala Ile Ala Glu Lys Pro Glu Pro Lys 515 520 S21 S25 Lys Asp Met Pro Met Pro Gly Gly Gly Gly Met Gly Gly Met Gly Gly Met 530 480 4211> 306 4211> 306 4212> DNA 4213 480 480 480 480 480 480 480 48		42	`				425					430			
450	Asp Asp	Asp Gl		Ala	Gly			Ile	Ile	Arg			Leu	Glu	
465		Leu Ar	g Gln	Ile		Ala	Asn	Ala	Gly		Glu	Gly	Ser	Ile	
Lys Lys Val Thr Arg Ile Ala Leu Gln Asn Ala Ala Ser Val Ala Ser 510 Leu Leu Leu Thr Thr Glu Cys Ala Ile Ala Glu Lys Pro Glu Pro Lys 525 Lys Asp Met Pro Met Pro Gly Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Say Met Gly Met Say Met Fro Glu Pro Lys 530 Asp Gly Met Tyr	465	_		470			_	_	475		_			480	
Leu Leu Leu Thr Thr Glu Cys Ala Ile Ala Glu Lys Pro Glu Pro Lys 515 Lys Asp Met Pro Met Pro Gly Gly Gly Met Gly Gly Met Gly Gly Met 530 Asp Gly Met Tyr 545		-	485		_			490		_			495		
Lys Asp Met Pro Met Pro Gly Gly Gly Met Gly Gly Gly Gly Met Gly Gly Met Gly		50) -				505					510			
Solo Solo Solo Solo Solo Solo Solo Solo		515			_	520					525			_	
<pre> <210> 3</pre>	_	Met Pro) Met	Pro	_	Gly	Gly	Met	Gly	_	Met	Gly	Gly	Met	
<pre><211> 306 <212> DNA <213> Lawsonia intracellularis </pre> <pre><220> <221> CDS <222> (1)(303) </pre> <pre><400> 3 atg dac ctg aaa cct ttg aat gac cgt gtt tta gta aaa cgt ctt gaa Met Asn Leu Lys Pro Leu Asn Asp Arg Val Leu Val Lys Arg Leu Glu 1</pre>		Met Ty	•												
<pre><211> 306 <212> DNA <213> Lawsonia intracellularis </pre> <pre><220> <221> CDS <222> (1)(303) </pre> <pre><400> 3 atg dac ctg aaa cct ttg aat gac cgt gtt tta gta aaa cgt ctt gaa Met Asn Leu Lys Pro Leu Asn Asp Arg Val Leu Val Lys Arg Leu Glu 1</pre>															
<pre><213> Lawsonia intracellularis <220> <221> CDS <222> (1)(303) <400> 3 atg aac ctg aaa cct ttg aat gac cgt gtt tta gta aaa cgt ctt gaa</pre>	<211> 30														
<pre> <221> CDS <222> (1)(303) <400> 3 atg aac ctg aaa cct ttg aat gac cgt gtt tta gta aaa cgt ctt gaa Met Asn Leu Lys Pro Leu Asn Asp Arg Val Leu Val Lys Arg Leu Glu 1</pre>			intr	acel:	lula	ris									
<pre><222> (1)(303) <400> 3 atg dac ctg aaa cct ttg aat gac cgt gtt tta gta aaa cgt ctt gaa Met Asn Leu Lys Pro Leu Asn Asp Arg Val Leu Val Lys Arg Leu Glu 1</pre>	<220>														
atg aac ctg aaa cct ttg aat gac cgt gtt tta gta aaa cgt ctt gaa 48 Met Asn Leu Lys Pro Leu Asn Asp Arg Val Leu Val Lys Arg Leu Glu 1)3)												
Met Asn Leu Lys Pro Leu Asn Asp Arg Val Leu Val Lys Arg Leu Glu 1	<400> 3														
tct gaa gaa aaa aca gct ggt gga ctc tat atc cct gat act gct aaa 96 Ser Glu Glu Lys Thr Ala Gly Gly Leu Tyr Ile Pro Asp Thr Ala Lys 30 gaa aaa cca tct cgt ggt gaa gtt gtt gct gtt gga cct ggt aaa cat 144 Glu Lys Pro Ser Arg Gly Glu Val Val Ala Val Gly Pro Gly Lys His 35 aca gat gat ggt aaa tta ata cct atg gct gta aaa gca gga gat aca 192 Thr Asp Asp Gly Lys Leu Ile Pro Met Ala Val Lys Ala Gly Asp Thr 50 gtt ctt ttt aat aag tat gca gga aca gaa gta aag ctt gat ggt gta 240 Val Leu Phe Asn Lys Tyr Ala Gly Thr Glu Val Lys Leu Asp Gly Val 65 gag cat cta gtt atg cgt gaa gat gac atc cta gct gtt att act gga 288 Glu His Leu Val Met Arg Glu Asp Asp Ile Leu Ala Val Ile Thr Gly 95 gaa act ggc cgc aag tga 306															48
Ser Glu Glu Lys Thr Ala Gly Gly Leu Tyr Ile Pro Asp Thr Ala Lys 20 25 30 30 30 30 30 30 30 30 30 30 30 30 30	1		5					10					15		
gaa aaa cca tct cgt ggt gaa gtt gtt gct gtt gga cct ggt aaa cat l44 Glu Lys Pro Ser Arg Gly Glu Val Val Ala Val Gly Pro Gly Lys His 45 aca gat gat ggt aaa tta ata cct atg gct gta aaa gca gga gat aca l92 Thr Asp Asp Gly Lys Leu Ile Pro Met Ala Val Lys Ala Gly Asp Thr 50 55 60 aca gaa gta aag ctt gat ggt gta Val Leu Phe Asn Lys Tyr Ala Gly Thr Glu Val Lys Leu Asp Gly Val 65 70 75 80 aca gaa gta act cta gtt atg cgt gaa gat gac atc cta gct gtt att act gga Glu His Leu Val Met Arg Glu Asp Asp Ile Leu Ala Val Ile Thr Gly 85 90 95 aca act ggc cgc aag tga 306	_	_		_											96
Glu Lys Pro Ser Arg Gly Glu Val Val Ala Val Gly Pro Gly Lys His aca gat gat ggt aaa tta ata cct atg gct gta aaa gca gga gat aca Thr Asp Asp Gly Lys Leu Ile Pro Met Ala Val Lys Ala Gly Asp Thr 50 S5 S S S S S S S S S S S S S S S S S		_			_	_		_			_			_	
aca gat gat ggt aaa tta ata cct atg gct gta aaa gca gga gat aca Thr Asp Asp Gly Lys Leu Ile Pro Met Ala Val Lys Ala Gly Asp Thr 50															144
Thr Asp Asp Gly Lys Leu Ile Pro Met Ala Val Lys Ala Gly Asp Thr 50 gtt ctt ttt aat aag tat gca gga aca gaa gta aag ctt gat ggt gta Val Leu Phe Asn Lys Tyr Ala Gly Thr Glu Val Lys Leu Asp Gly Val 80 gag cat cta gtt atg cgt gaa gat gac atc cta gct gtt att act gga Glu His Leu Val Met Arg Glu Asp Asp Ile Leu Ala Val Ile Thr Gly 85 gaa act ggc cgc aag tga 306	_	35				40					45				
gtt ctt ttt aat aag tat gca gga aca gaa gta aag ctt gat ggt gta Val Leu Phe Asn Lys Tyr Ala Gly Thr Glu Val Lys Leu Asp Gly Val 65															192
Val Leu Phe Asn Lys Tyr Ala Gly Thr Glu Val Lys Leu Asp Gly Val 65 70 75 80 gag cat cta gtt atg cgt gaa gat gac atc cta gct gtt att act gga Glu His Leu Val Met Arg Glu Asp Asp Ile Leu Ala Val Ile Thr Gly 85 90 95 gaa act ggc cgc aag tga 306	50		_		55					60					
gag cat cta gtt atg cgt gaa gat gac atc cta gct gtt att act gga Glu His Leu Val Met Arg Glu Asp Asp Ile Leu Ala Val Ile Thr Gly 85 90 95 gaa act ggc cgc aag tga 306	-		_		-	-		_	-						240
Glu His Leu Val Met Arg Glu Asp Asp Ile Leu Ala Val Ile Thr Gly 85 90 95 gaa act ggc cgc aag tga 306	65			70					75					80	
gaa act ggc cgc aag tga 95															288
		DCG VG				-	-								
100		Dou va						90					95		

```
<210> 4
<211> 101
<212> PRT
<213> Lawsonia intracellularis
Met Asn Leu Lys Pro Leu Asn Asp Arg Val Leu Val Lys Arg Leu Glu
                                    10
Ser Glu Glu Lys Thr Ala Gly Gly Leu Tyr Ile Pro Asp Thr Ala Lys
            20
                                25
Glu Lys Pro Ser Arg Gly Glu Val Val Ala Val Gly Pro Gly Lys His
                            40
Thr Asp Asp Gly Lys Leu Ile Pro Met Ala Val Lys Ala Gly Asp Thr
                        55
Val Leu Phe Asn Lys Tyr Ala Gly Thr Glu Val Lys Leu Asp Gly Val
                    70
                                        75
Glu His Leu Val Met Arg Glu Asp Asp Ile Leu Ala Val Ile Thr Gly
                                    90
Glu Thr Gly Arg Lys
            100
<210> 5
<211> 4972
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> misc feature
<222> (1)...(4972)
<223> n = A, T, C or G
<400> 5
aactcctggt ctatcaagat caactaaaaa atattcttta tctaatagtt gctcaaaaat 60
aattgtacct acaggtaaat gaagaatcaa atcttcccct tttttaccat gacgctggct 120
ccctttacca ccttctccat tttgagctct atagtgacgt tgcacacgaa aatcataaag 180
ggttaacaaa cgtgaatcag ctttaaaaat tatattacct ccatctcctc catccctcc 240
attaggtcca cctttaggta taaacttttc gcgtctaaat gaaacacatc catttccacc 300
ttttcctgcg ctcacgctaa tagttacttc atcaacaaaa cgcatgatta tcctttcaat 360
aacaaatatc tattcaatac tgttactaac ttgtttactg ttttttctag aaaattacct 420
ggctaattat tatagttata tctagattaa tgaaaaagga agaagtcatt acactccttc 480
cttattaata gaatcctgga ataattatta tacggtgggt tgtatatgca ctctactata 540
tcttttacat ttacqaaaat atqtttcata aqttactata ccattaactt ttqcaaataa 600
agtatagtct cttcccattc caacattttc tccaggatga atttttgtac ctagttgacg 660
aacaaggata ttgcctgcca agactttctg gccgccgaaa cgctttatac cacgacgttg 720
tectggaeta tetetaceat tgcgagaact tecaceaget ttettatggg ceattttaat 780
atctccttaa agctgaatac ctgttacttt tagagctgta tagtcttgac gatgaccttg 840
gagtttacgt gagtcatttc ttctccactt tttaaaaaca agaatttttt tatcacgacc 900
atgctcaaga actttagcta taactttagc attattaata tatggtgttc caatttgagg 960
agatgaacca ccaatcataa aaattttatc aaaaaaaatt tctgttccaa cttcagcgtc 1020
tattttagaa acaaaaattt tagaaccctc ttcaacacag aattgttttc caccagcttc 1080
aataattgcg tacataaata atgtgcctcc caaaaaagac aagaaatact aatttgatat 1140
tttcaatatt gtcaagtagg aactttatct ttagaatgtt agatgtaaca atttttttag 1200
aaaaaaaata ttttcaatac aataggaaaa gaggaaaaaa aaaaagattt ttagaaaaaa 1260
tttttatttc tccaaaaaat gcaaaaatat aaaaaattct aataggatag aagttattac 1320
tgtattgatt ttcaagactt acttaaaaat ttttataaaa aaatttgcat tcccctcttc 1380
```

ccaattccca tagagaagat tatttatcct aacgattggt ggacgctaag tccctgctgt 1440 tttgattata tatcaaatgt tgaaacaaat tttgtttagt ttctttttgt actctaaaaa 1500 gaagacaaaa aattetttat aaactgtaca etetaaacaa aatagtteae aataaacage 1560 aatacattat aattaattgg aggatactat tgtcatgaac ctgaaacctt tgaatgaccg 1620 tgttttagta aaacgtcttg aatctgaaga aaaaacagct ggtggactct atatccctga 1680 tactgctaaa gaaaaaccat ctcgtggtga agttgttgct gttggacctg gtaaacatac 1740 agatgatggt aaattaatac ctatggctgt aaaagcagga gatacagttc tttttaataa 1800 gtatgcagga acagaagtaa agcttgatgg tgtagagcat ctagttatgc gtgaagatga 1860 catcctagct gttattactg gagaaactgg ccgcaagtga aaaaggcgta aataaaaaqa 1920 tcggtgatct ttaataattt tattcagtta taatgaaaac actaattaca cgcactctct 1980 qagaattttc tcagaaaact atatttaaca attctaaaat cgatatgttt ttaggaggaa 2040 aaccctaatg gcttctaaag aaatcctttt tgatgctaaa gcccgtgaaa aactttcacg 2100 aggtgtagat aaacttgcaa atgctgttaa agtaacactt ggacctaaag qccgtaatgt 2160 cgttattgaa aagtcttttg gttccccagt tattacaaaa gatggtgtat ctgttgcaaa 2220 agaaattgaa cttgaagata agtttgaaaa tatgggcgct caaatggtta aagaagtagc 2280 tcccaaaact agcgatattg ctggtgatgg aactacaaca gcaacagtcc ttgcacaagc 2340 tatttatcgt gaaggtgtaa aacttgtagc agctggtcgt aatcctatgg ccattaaacg 2400 tggcatagat aaagctgttg ttgctgttac taaagaacta agcgacatta caaagcctac 2460 tcgtgaccaa aaagaaatag ctcaagttgg aaccatttct gcaaactctg atacaacaat 2520 aggtaatatc atagctgaag ctatggctaa agttggaaaa ggaggtgtta tcacagttga 2580 ggaagctaaa ggtcttgaaa ctacattaga tgtggttgaa ggaatgaagt ttgaccgtgg 2640 ctacctctct ccatactttg taactaatcc tgagaaaatg gtttgtgaac ttgataaccc 2700 ttatatcctt tgtaatgaga aaaagattac tagcatgaaa gacatgctac caatcttaga 2760 acaagttqct aaaqtaaacc qtccactcct tattattqct qaaqacqtaq aaggtqaaqc 2820 acttgcaaca cttgtagtca ataagctccg tggagcactc caagttgtag ccgtaaaagc 2880 tcctggtttt ggtgaacgcc gtaaagctat gcttgaagat attgctatcc ttactggagg 2940 agaagcaata tttgaagatc gtggtataaa gcttgaaaat gtaagcttgt cttctttagg 3000 aacagctaaa cgtgtagtta ttgacaaaga aaatactact atcgttgatg gtgctggaaa 3060 atcaqaaqat attaaaqctc qaqttaaaca aattcqtqca caaattqaaq aaacaaqctc 3120 agattatgat cgtgaaaaac ttcaagaacg tcttgcaaaa cttgttggtg gagtagctgt 3180 tatccatgtt ggagctgcta ctgaaactga aatgaaagag aagaaggatc gtgtagaaga 3240 tgctctaaat gcaacaagag ctgcggttga agaaggtatt gtccctggtg gtggtactqc 3300 ttttgtccgc tccattaaag tccttgatga tattaaacct gctgatgatg atgaacttgc 3360 tggacttaat atcatccgtc gttctcttga agagccttta cgtcaaattg ctgcaaatgc 3420 tggctatgaa ggttctattg ttgtagaaaa agttcgtgaa ccaaaagatg gttttggatt 3480 taatgctgca tcaggagaat atgaagacct tattaaagct ggtgtcattg atcctaaaaa 3540 agttacacgt attgcattac aaaatgcagc atcagtagcc tccttacttc taactacaga 3600 atgcgctatt gctgaaaaac cagaacctaa aaaagatatg cctatgcctg gcggtggtat 3660 gggtggtatg ggtggtatgg acggtatgta ctagtcctat cttcagtaca acttagatgt 3720 ataaaaaccc cagaagcaat gcttccgggg ttttatactt tcagcataaa aaattaatat 3780 ttaatataca gacacattat tttggtattt attatttatt atgatcaaat atatagactg 3840 gatacaaaaa acaacaatga tgtttaaaaa ggcagggata gattcaccaa aactctctgc 3900 agaacttata ttaagtcatg ttttaaatat tacacgatta caaataataa tgactccttt 3960 tgaacctatt ccaactaata gctactcaac gcttaatgat atcatgttaa gaagactcca 4020 tggagaacca attgcatatc tcacagggaa aaaagaattt ttttcacgag aatttaaagt 4080 cactcaaqcc acacttatcc ctcqcccaqa qacaqaqtta cttataqaat ttqtattaaa 4140 ccatattaac ccaacacaac aaatatactt tqcaqactta qqtacaqqta qtqqqtqtat 4200 tgcaattaca ctagctgctg aaagaaaaaa ttggttaggt attgctactg atatctctag 4260 tgaagcatta aaaatagcta aacttaatag tttaaaaaaat aacactcata gtcaactaca 4320 gtttcttcaa tcagatttta cacaaccact ctgtctaccc tcttcattag acttatatat 4380 cagtaatcct ccatatataa gtgaaaatga actgacctct cttccgcatg aagtaatatc 4440 ttttgaacct aaaatagctc ttacaccaca taaatgtatt catcttgatg aaataaatac 4500 cgttttacac tgctataaaa aaattattac ccaagcagag atatccctta agcctggagg 4560 aataataatt ttagaacatg gagcaacaca agcagaagct atcttattqt tgttaaaaaa 4620 caacatatgg acaaatgtaa taagtcatac tgatcttaca aataaaaatc gttttattac 4680 agcatataag tataaaatat aacttaatta tgttgkagaa aaaacaaaaa ataaaaataa 4740 gatattaaat attttttta ataaaattaa gcaattacta atatcttttt ttggrtcgtt 4800

	4860 4920 4972										
<210> 6 <211> 569 <212> DNA <213> Lawsonia intracellularis											
<220> <221> CDS <222> (209)(244)											
<221> CDS <222> (248)(568)											
<pre><221> misc_feature <222> (1)(569) <223> n = A,T,C or G</pre>											
<pre><400> 6 ggttaaaaag taaggagaaa aggttggtta aaccaagttt aaaaaattaa tttttttta 6 ttacccaaaa aagtttatta gattaagtaa tattaatttg gcccaaaaat ttttttgggc 1 atgggtttt tgcttttaaa atagagatgt gtaggtaaca ttttttcctc catgaaatta 1 ttttttagga gatgttatca tgatgggg agt ttg ttt att gnt gcg aac agg 2 Ser Leu Phe Ile Xaa Ala Asn Arg 1 5</pre>	120										
tat gaa aac cca tag nac agg gnt ggt act gtc tcc aat aat att gct 2 Tyr Glu Asn Pro Xaa Arg Xaa Gly Thr Val Ser Asn Asn Ile Ala 10 15 20	280										
aac gca aat acc att ggg tat aag cag caa cag gta gtg ttt caa gac Asn Ala Asn Thr Ile Gly Tyr Lys Gln Gln Gln Val Val Phe Gln Asp 25 30 35	328										
ctg ttt agt caa gat tta gca ata ggt ttt act gga agt cag ggg cca Leu Phe Ser Gln Asp Leu Ala Ile Gly Phe Thr Gly Ser Gln Gly Pro 40 55	376										
aac cag gct ggt atg gga gca cag gtg gga agt gtt cgc aca att ttt 4 Asn Gln Ala Gly Met Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe 60 65 70	424										
aca cag ggt gct ttt gaa cct ggc aat agt gta aca gat cct gct att Thr Gln Gly Ala Phe Glu Pro Gly Asn Ser Val Thr Asp Pro Ala Ile 75 80 85	472										
ggt gga aaa ggt ttt ttt cag gtt aca tta gag gat aaa gta cac tat Gly Gly Lys Gly Phe Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr 90 95 100	520										
aca cga gca ggg aat ttt cgt ttt act caa gat ggt ttt tta aat gat Thr Arg Ala Gly Asn Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp 105 110 115	568										
c 5	569										

```
<210> 7
<211> 12
<212> PRT
<213> Lawsonia intracellularis
<220>
<221> VARIANT
<222> (1)...(12)
<223> Xaa = Any Amino Acid
<400> 7
Ser Leu Phe Ile Xaa Ala Asn Arg Tyr Glu Asn Pro
<210> 8
<211> 107
<212> PRT
<213> Lawsonia intracellularis
<220>
<221> VARIANT
<222> (1)...(107)
<223> Xaa = Any Amino Acid
<400> 8
Xaa Arg Xaa Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile
                                    10
Gly Tyr Lys Gln Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp
Leu Ala Ile Gly Phe Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met
                            40
Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe
                        55
Glu Pro Gly Asn Ser Val Thr Asp Pro Ala Ile Gly Gly Lys Gly Phe
                    70
                                        75
Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn
Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp
            100
<210> 9
<211> 1450
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> CDS
<222> (3)...(410)
<221> CDS
<222> (1080)...(1448)
<221> misc_feature
<222> (1)...(1450)
```

<223> n = A, T, C or G

Ser Lys Glu Ser Thr Tyr Ile Ala Arg Ile Glu Asn Ser Thr Ser	47
gaa aaa aca cta aat gat ctt gat ata ctt tta aaa gat gtg atg tta Glu Lys Thr Leu Asn Asp Leu Asp Ile Leu Leu Lys Asp Val Met Leu 20 25 30	95
aca tca aaa aag cat gaa tca cgt aga ctt gca gag tct gta cat caa Thr Ser Lys Lys His Glu Ser Arg Arg Leu Ala Glu Ser Val His Gln 35 40 45	143
aat att ctt acc cac ctt ata caa aaa aat tat aat a	191
ggg ata aaa tct gca cct ttt cat gtt ctt ata gga ccc aaa ata cca Gly Ile Lys Ser Ala Pro Phe His Val Leu Ile Gly Pro Lys Ile Pro 65 70 75	239
agt att ctt gtt gaa gta ggt tac tgt agt aat aaa gct gaa gca cag Ser Ile Leu Val Glu Val Gly Tyr Cys Ser Asn Lys Ala Glu Ala Gln 80 85 90 95	287
cgt ctg gca tct agt aat tac caa aaa gca tta ata gaa gga tta gct Arg Leu Ala Ser Ser Asn Tyr Gln Lys Ala Leu Ile Glu Gly Leu Ala 100 105 110	335
aaa ggt att ttc tgt tac cta aaa aaa cta cat cac ctt gat att tac Lys Gly Ile Phe Cys Tyr Leu Lys Lys Leu His His Leu Asp Ile Tyr 115 120 125	383
tct agt ttt aty cta tct aat tgc act taatagcttg gacaattatt Ser Ser Phe Xaa Leu Ser Asn Cys Thr 130 135	430
atatgaaggg tatccatgtg aaggtacctg gttaagcttt taaatgtaaa aattatgcaa 4 ccatacytta ttccttcaga ggagcttcat tatgaaagta aaaactcttt ccatggctat 5 tttagcttgt ttattagtag ctaacagtge attttcggct gacttcccta ttggtgtctt 6 taattctcaa tccattgcca tggagagtga agcagctaag gccgctcaaa aaaaattaca 6 atcagaattt ggtaatgaaa aaacacaact tgaaaacaag caaaagwttg cmaacaaaaag ctgatgattt acaagctwag tcagcagcta tgtytaacca agcacgtgaa gataaacaaa 6 aagaatttct tgaacttcgt cgtaatttcg aagaaaaaty tcgtgacttt gcaatacgtg 6 tcgaacaagc tgaaaacaca ttacgtcaat atntagctga acaaatntat nttgctgctg 6 aaactatagc aaaaaagaaa gggttaaact tgttttgata gtgttaggga agtgtaatgt 6 accttgaaaa aaatttagat attacaaaga aattyttgaa gccataaatg ctgcatggaa 1 aaaaggtgga agtaaacttc cagagatggc aaaccggaaa aaataacag atg ccc cag 1 Met Pro Gln	550 610 670 730 790 850 910 970
tat aaa ctt tca gaa att gct aaa ctt tta aac tta aca tta caa ggt Tyr Lys Leu Ser Glu Ile Ala Lys Leu Leu Asn Leu Thr Leu Gln Gly 140 145 150 150	1136

```
gat gat att gaa gtt gta ggc gta aat aca ctt caa gat gca tca cca
                                                                   1184
Asp Asp Ile Glu Val Val Gly Val Asn Thr Leu Gln Asp Ala Ser Pro
                                     165
aat gag ata agt ttt cta gca aat gct aaa tat att cac cag ctt gtt
                                                                   1232
Asn Glu Ile Ser Phe Leu Ala Asn Ala Lys Tyr Ile His Gln Leu Val
                                 180
ttg tca cag gct ggt gct att att ctt tca aaa gaa tat gct agt cgt
                                                                   1280
Leu Ser Gln Ala Gly Ala Ile Ile Leu Ser Lys Glu Tyr Ala Ser Arg
        190
                            195
gtt cca cga gca cta atc agt act gaa cca tat aga gat ttt ggt aga
                                                                   1328
Val Pro Arg Ala Leu Ile Ser Thr Glu Pro Tyr Arg Asp Phe Gly Arg
    205
                        210
gtt ctt tct tta ttc tct ata cct caa gga tgt ttt gat ggt ata agt
                                                                   1376
Val Leu Ser Leu Phe Ser Ile Pro Gln Gly Cys Phe Asp Gly Ile Ser
220
                    225
                                                             235
cat caa gct tat ata cac cct aca gca caa gtc tct aaa aca gct act
                                                                   1424
His Gln Ala Tyr Ile His Pro Thr Ala Gln Val Ser Lys Thr Ala Thr
                240
                                     245
atc tat cct ttn gtt ttt ata gga tc
                                                                   1450
Ile Tyr Pro Xaa Val Phe Ile Gly
            255
<210> 10
<211> 136
<212> PRT
<213> Lawsonia intracellularis
<220>
<221> VARIANT
<222> (1)...(136)
<223> Xaa = Any Amino Acid
<400> 10
Ser Lys Glu Ser Thr Tyr Ile Ala Arg Ile Glu Asn Ser Thr Ser Glu
                 5
                                     10
Lys Thr Leu Asn Asp Leu Asp Ile Leu Lys Asp Val Met Leu Thr
                                 25
Ser Lys Lys His Glu Ser Arg Arg Leu Ala Glu Ser Val His Gln Asn
                            40
Ile Leu Thr His Leu Ile Gln Lys Asn Tyr Asn Thr His Asn Gly Gly
Ile Lys Ser Ala Pro Phe His Val Leu Ile Gly Pro Lys Ile Pro Ser
                    70
                                         75
Ile Leu Val Glu Val Gly Tyr Cys Ser Asn Lys Ala Glu Ala Gln Arg
Leu Ala Ser Ser Asn Tyr Gln Lys Ala Leu Ile Glu Gly Leu Ala Lys
                                105
            100
                                                     110
Gly Ile Phe Cys Tyr Leu Lys Lys Leu His His Leu Asp Ile Tyr Ser
                            120
Ser Phe Xaa Leu Ser Asn Cys Thr
```

130 135

<210> 11

```
<211> 123
<212> PRT
<213> Lawsonia intracellularis
<220>
<221> VARIANT
<222> (1)...(123)
<223> Xaa = Any Amino Acid
<400> 11
Met Pro Gln Tyr Lys Leu Ser Glu Ile Ala Lys Leu Leu Asn Leu Thr
Leu Gln Gly Asp Asp Ile Glu Val Val Gly Val Asn Thr Leu Gln Asp
            20
                                25
Ala Ser Pro Asn Glu Ile Ser Phe Leu Ala Asn Ala Lys Tyr Ile His
                            40
Gln Leu Val Leu Ser Gln Ala Gly Ala Ile Ile Leu Ser Lys Glu Tyr
                        55
Ala Ser Arg Val Pro Arg Ala Leu Ile Ser Thr Glu Pro Tyr Arg Asp
                    70
                                         75
Phe Gly Arg Val Leu Ser Leu Phe Ser Ile Pro Gln Gly Cys Phe Asp
                                     90
                85
Gly Ile Ser His Gln Ala Tyr Ile His Pro Thr Ala Gln Val Ser Lys
                                105
Thr Ala Thr Ile Tyr Pro Xaa Val Phe Ile Gly
        115
                             120
<210> 12
<211> 559
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> CDS
<222> (3)...(296)
<221> CDS
<222> (300)...(557)
<221> misc feature
<222> (1)...(559)
<223> n = A, T, C or G
<400> 12
                                                                   47
ga tca aag ccg cat tta cng caa gag tta gaa att gaa gtt ttg aaa
   Ser Lys Pro His Leu Xaa Gln Glu Leu Glu Ile Glu Val Leu Lys
aaa gaa gac ttt ggg cgt cat att gtt aaa tta tgc tgg aaa ggt tct
Lys Glu Asp Phe Gly Arg His Ile Val Lys Leu Cys Trp Lys Gly Ser
                 20
```

tta tca aat atc ttt ttt tcc tat ggg gat atc ccg cac cca cct tat Leu Ser Asn Ile Phe Phe Ser Tyr Gly Asp Ile Pro His Pro Pro Tyr 35 40 45	143									
ata cat caa agt aat aag gtt cag gat aag gaa aga tat cnt acn gta Ile His Gln Ser Asn Lys Val Gln Asp Lys Glu Arg Tyr Xaa Thr Val 50 55 60	191									
tac tct ata tta cat aan ctg ggt tct gta gca gct cct aca gct gga Tyr Ser Ile Leu His Xaa Leu Gly Ser Val Ala Ala Pro Thr Ala Gly 65 70 75	239									
tta cnc ttt tct gaa act agc cgt nat aaa tta cac aaa nat ggt att Leu Xaa Phe Ser Glu Thr Ser Arg Xaa Lys Leu His Lys Xaa Gly Ile 80 85 90 95	287									
agt tgg gca taa atc cct ctt cac gtg gga tat gga aca ttc agt ccc Ser Trp Ala Ile Pro Leu His Val Gly Tyr Gly Thr Phe Ser Pro 100 105 110	335									
gtc ctc tgc aat gac atc cca aaa cat ctt atc cnt tct gag ttt gtt Val Leu Cys Asn Asp Ile Pro Lys His Leu Ile Xaa Ser Glu Phe Val 115 120 125	383									
cac ttt cct gaa act acn ttt tcc act ata tta aat gca cgg ttt gca His Phe Pro Glu Thr Thr Phe Ser Thr Ile Leu Asn Ala Arg Phe Ala 130 135 140	431									
ngg gaa tac cta tgt tct gcc ata ggg gac cca ctg ttg tcc cca cca Xaa Glu Tyr Leu Cys Ser Ala Ile Gly Asp Pro Leu Leu Ser Pro Pro 145 150 155	479									
ttg gan ggg tgt tat ctt acc cct ttc gcc cgg ggt tcc cct ccc caa Leu Xaa Gly Cys Tyr Leu Thr Pro Phe Ala Arg Gly Ser Pro Pro Gln 160 165 170	527									
ccc tat tcc att gng ttt tcc tct caa att at Pro Tyr Ser Ile Xaa Phe Ser Ser Gln Ile 175 180	559									
<210> 13 <211> 98 <212> PRT <213> Lawsonia intracellularis										
<220> <221> VARIANT <222> (1)(98) <223> Xaa = Any Amino Acid										
<400> 13 Ser Lys Pro His Leu Xaa Gln Glu Leu Glu Ile Glu Val Leu Lys Lys										
1 5 10 15 Glu Asp Phe Gly Arg His Ile Val Lys Leu Cys Trp Lys Gly Ser Leu										
20 25 30 Ser Asn Ile Phe Phe Ser Tyr Gly Asp Ile Pro His Pro Pro Tyr Ile										

```
40
        35
His Gln Ser Asn Lys Val Gln Asp Lys Glu Arg Tyr Xaa Xaa Val Tyr
                                             60
                        55
Ser Ile Leu His Xaa Leu Gly Ser Val Ala Ala Pro Thr Ala Gly Leu
                                        75
Xaa Phe Ser Glu Thr Ser Arg Xaa Lys Leu His Lys Xaa Gly Ile Ser
                                     90
Trp Ala
<210> 14
<211> 86
<212> PRT
<213> Lawsonia intracellularis
<220>
<221> VARIANT
<222> (1)...(86)
<223> Xaa = Any Amino Acid
<400> 14
Ile Pro Leu His Val Gly Tyr Gly Thr Phe Ser Pro Val Leu Cys Asn
                                     10
Asp Ile Pro Lys His Leu Ile Xaa Ser Glu Phe Val His Phe Pro Glu
            20
                                25
Thr Xaa Phe Ser Thr Ile Leu Asn Ala Arg Phe Ala Xaa Glu Tyr Leu
Lys Ser Ala Ile Gly Asp Pro Leu Leu Ser Pro Pro Leu Xaa Gly Cys
Tyr Leu Thr Pro Phe Ala Arg Gly Ser Pro Pro Gln Pro Tyr Ser Ile
65
Xaa Phe Ser Ser Gln Ile
                85
<210> 15
<211> 477
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> CDS
<222> (2)...(10)
<221> CDS
<222> (14)...(178)
<221> CDS
<222> (182)...(220)
<221> CDS
<222> (224)...(256)
<221> CDS
<222> (269)...(295)
```

```
<221> misc feature
<222> (1)...(477)
<223> n = A, T, C or G
<400> 15
t ata aaa cat tag cgn ctt tng tat ttg gac ttc aaa aaa att ttt aat 49
  Ile Lys His Arg Leu Xaa Tyr Leu Asp Phe Lys Lys Ile Phe Asn
tat ata gga gaa cat tca cca tta aaa cgt aat gta ant atg gaa gat
                                                                   97
Tyr Ile Gly Glu His Ser Pro Leu Lys Arg Asn Val Xaa Met Glu Asp
                                     25
gta ggt aaa tot got gtt ttt tta got toa gao otn toa toa gga gta
                                                                   145
Val Gly Lys Ser Ala Val Phe Leu Ala Ser Asp Leu Ser Ser Gly Val
acc ggt gaa ttn ttt ttg ttg atg ctg gna caa taa ttt agg tat tta
                                                                   193
Thr Gly Glu Xaa Phe Leu Leu Met Leu Xaa Gln Phe Arg Tyr Leu
         50
                             55
acc ata cat gct tta tac aac ata ttg tga gtt aca ata gcc ata aca
                                                                   241
Thr Ile His Ala Leu Tyr Asn Ile Leu Val Thr Ile Ala Ile Thr
                             70
cat tta tat tct ata taataacagt ag aat aat aga ata ttt ttt atg 292
His Leu Tyr Ser Ile
                                 Asn Asn Asn Arg Ile Phe Phe Met
         80
                                          85
acc atttgtatct atacaatagt aaatagatta atacatataa gactatattc
                                                                  345
Thr
tttttgagag caacttaaag gagcggttat ggctttagtt acaaaagaag aagtacttca 405
ataccatagt gaaccccgac caggtaaact tgaagtattt tctataaaac catgtaaaac 465
acaaaaagat cc
                                                                   477
<210> 16
<211> 3
<212> PRT
<213> Lawsonia intracellularis
<400> 16
Ile Lys His
1
<210> 17
<211> 55
<212> PRT
<213> Lawsonia intracellularis
<220>
<221> VARIANT
<222> (1)...(55)
<223> Xaa = Any Amino Acid
```

```
<400> 17
Xaa Leu Xaa Tyr Leu Asp Phe Lys Lys Ile Phe Asn Tyr Ile Gly Glu
 1
                                     10
His Ser Pro Leu Lys Arg Asn Val Xaa Met Glu Asp Val Gly Lys Ser
            20
                                25
Ala Val Phe Leu Ala Ser Asp Xaa Ser Ser Gly Val Thr Gly Glu Xaa
                             40
Phe Leu Leu Met Leu Xaa Gln
    50
<210> 18
<211> 13
<212> PRT
<213> Lawsonia intracellularis
<400> 18
Phe Arg Tyr Leu Thr Ile His Ala Leu Tyr Asn Ile Leu
         5
                                     10
<210> 19
<211> 11
<212> PRT
<213> Lawsonia intracellularis
<400> 19
Val Thr Ile Ala Ile Thr His Leu Tyr Ser Ile
<210> 20
<211> 9
<212> PRT
<213> Lawsonia intracellularis
<400> 20
Asn Asn Asn Arg Ile Phe Phe Met Thr
                 5
<210> 21
<211> 525
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> CDS
<222> (2)...(352)
<221> CDS
<222> (356)...(361)
<221> CDS
<222> (365)...(409)
<221> CDS
```

<22	2> (4	113).	(4	133)												
	1> CI 2> (4	-	(4	151)												
	L> CI 2> (4		(5	523)												
g ga G		g tt		al Ph					cg Se					p Le	a ctt eu Leu 15	49
			att Ile 20						_							97
			agc Ser													145 .
	-	_	gct Ala			_			_			_	_	-		193
_		_	gtt Val													241
			ttt Phe									-				289
-	-		ttt Phe 100		-	_							_		_	337
_			tat Tyr			aaa Lys <i>P</i>	-	_	eu Va	-	aag /s I]			/r Il		385
			tac Tyr 130					I			act Thr]		Chr S			433
tga			gat Asp	_			aga Arg ('yr I			_	_	1et I	-	481
			tgt Cys					-	_		_					523
cc																525
)> 22 L> 11															

```
<212> PRT
<213> Lawsonia intracellularis
<400> 22
Glu Leu Leu Val Phe Ser Gln Asn Arg Ser Gln Asn Ile Trp Leu Leu
               5
                                   10
Thr Leu Pro Ile Phe Val Leu Gly Ile Ala Gln Gly Ile Ser Phe Pro
Leu Val Asn Ser His Ile Thr Ser Leu Ala Pro Thr Ser Asn Arg Ala
                            40
Ile Val Met Ala Ile Asn Ser Thr Phe Met Arg Leu Ser Gln Ser Ile
                        55
Ser Gln Met Val Phe Gly Ile Gly Trp Ser Phe Phe Gly Trp Pro Gly
                    70
Pro Phe Ile Phe Gly Leu Phe Thr Ser Ile Ile Leu Ala Leu Leu Ile
Met Lys Tyr Phe Gln Asp Val Thr Gln Tyr His Leu Phe Leu Ile Ser
           100
                               105
Ser Lys Phe Tyr Tyr
       115
<210> 23
<211> 2
<212> PRT
<213> Lawsonia intracellularis
<400> 23
Lys Ala
1
<210> 24
<211> 15
<212> PRT
<213> Lawsonia intracellularis
<400> 24
Leu Val Lys Ile Thr Tyr Ile Ile Tyr Asn Tyr Tyr Asn Ile Asn
                                    10
<210> 25
<211> 7
<212> PRT
<213> Lawsonia intracellularis
<400> 25
Leu Leu Thr Ile Thr Ser Asn
<210> 26
<211> 5
<212> PRT
<213> Lawsonia intracellularis
```

```
<400> 26
Leu Ile Asp Ala Ile
 1
<210> 27
<211> 23
<212> PRT
<213> Lawsonia intracellularis
<400> 27
Arg Gly Tyr Ile Asn Asp Val Met Ala His Asn Arg Cys Tyr Pro Trp
Ile Ser Ala Trp Asp Pro Gly
            20
<210> 28
<211> 846
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> misc feature
<222> (1)...(846)
<223> n = A, T, C or G
<400> 28
tatttactcg cgcggccggg cgtcttacac aaatggatcc cttgcantaa tccaaggata 60
acncetattg tganceatga acateatean natateetet ttanatagea tenannnnte 120
aannggaatt aacagttact anntagttaa tgtcatagta attgtcnata atatatgtaa 180
tcttaactaa ctaagctnnt taataataaa attnactact tatcaanaat aggtgatatn 240
gggttacatc ttgaaaatac ttnccataat tangagggct aatataatng aantaaaaag 300
accanatata aaaggaccag gccaaccaaa aaatgaccat ccaataccna aaacaattgg 360
cqaaaatact ctqacttaac ctcanaaatq tactqtttat aqccatatca ataqctctqt 420
tggatgtngg ngcaattgat gtaatgtggc tgtntactan angaaatgat ntacctcgtg 480
ctatnectan nacaanaata ngtaatgtaa gtaneenaat atettggett tgtaatggga 540
gaataatnnc aagtccttgg gaaatnaant tacnnccagc cagctatnnt aagcagttct 600
ntggtgacta tacgtcctac tnaantcgtg ccaaagatta aatanncgat aatcgcnctn 660
cctaaancan gcaatactaa aatggtttct ncctancttg gnatanggtg gaagenegga 720
cagaattnan ttcgcnantt tanannggaa natncgtnaa nttantcggg gcccannccn 780
aaatteetna ntenatanan naaetnnetn etntaaaang geenaetgga ntngttaaat 840
qaaata
<210> 29
<211> 855
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> misc_feature
<222> (1)...(855)
<223> n = A, T, C or G
<400> 29
gattntttat cgatcactnt agacgcgatt tgggnaacac ttacctggta nccacccggg 60
tggaaaaatc gatgggcccg cggccgctct agaagtactc tcgagaagct ttttgaattc 120
```

```
tttggatcct caacacaggg tatggattaa aacaacttta gctctaacag gagcatttta 180
taatatattc cctggtagaa caatatctac tcaagaaaat ctgtctattg gttttcaact 240
aaaaaaaact tttaaacctt ttcattggac catcttactc ttagatgaac attatatgtc 300
ttcgccaaga attgcagcag caattatgcc tgcacagctt gctggagtta aaaacattat 360
agctgtttgg accagtaaaa ataaccgact gaccgctgaa aaaatctcac ctgctttact 420
aacaacatta gaactttcag gagttaacat agccctaaca cttacccaca ctgaaactga 480
acttcttatt catcaattaa tgaaaatagg tattggaaac ctgttatatt ttttaaaaga 540
agaagacata ctacatatat ctactatacc tgtactacct ttctggaaag aatatacttc 600
tcatcgactt gttatagaaa aagatgctgg cnttaataca gaaatcctcc aatgggcnca 660
tcctcattca attattgaac aaatagcaac agaaccatac tctgaaanat atcccagatg 720
cactttactg tgctagctca tccantaaaa actatnctca tanagnatcc ccagaatttt 780
tcatnatgga cttgaaccta tttggattca ncccaacnet teetecaane eteettete 840°
catacaccat gggga
                                                                   855
<210> 30
<211> 1082
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> misc feature
<222> (1)...(1082)
<223> n = A, T, C or G
<400> 30
tatctngttg antcaataaa acttttgggg cccntnaaan tttcatnann aaaaaaacaa 60
nattnetggg ggnecentee caaaaaanne aateantnng aanettgnet tettattnng 120
nttttnanac tataatatnt nttatcnata atnnatcnnt atactnattt ctnattcant 180
nacannggnn agnaanntta atctnaaana ctncnaaggg ggnnntnata ntntttnttt 240
ntttntcccn tnnaatnnat aaccnnncac ccnnattant tnnaatnnat accatancnn 300
cctttcaaac tgtacacata ntannnaann acactcnanc nttttncatc ctctctantn 360
conacteona tnnanctntt occecatnoe tatntntone tgetteecag nttnnacntn 420
nettnnttte acantattee tatecaanet aacatntntn ntntentnet eettntntnt 480
tatntntttc tnntacctnn cactgacant ctatnantna nntcnnatac tnntatanct 540
ntangenant ntatetanaa ntntanennn nnatentnae ngeegtnnat ntnnnnnean 600
ttanntannn ctancntnnc caannncnta tntatnaata acnactatcc natattnnat 660
tnnntnntnt cntanncaaa tnatttangc ncacnncact angtnatatn annattntat 720
attntgaanc ttctnggctt cncnaatant accantnnnc anchtcnnnt ncatctnnnt 780
ntacttenta ecataneget etenagnnte actaetteta ntagtnaten tetaetgeen 840
atggennnnn gennnnegan agntatneae ntaeantnne ntetaetatn tanatetann 900
nenteegning cetnengtae gintingena antegnitae tetnentita tetagtenea 960
tcagnnntng antcctcaan cnngctctan ttacatgtnn nntnatgcnc tanancgnna 1020
cntctatcct tcnantctgc nctnantnta tanactctnn nnnatcnncn aanctatntc 1080
CC
                                                                   1082
<210> 31
<211> 354
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> misc feature
<222> (1)...(354)
<223> n = A, T, C or G
<400> 31
ctcccntnnc nctaagtgga ntcgcgcgct gcaggtcgac actagtggat cttqatatac 60
```

```
ttttaaaaqa tqtgatgtta acatcaaaaa agcatgaatc acgttagact tgcagagtct 120
qtacatcaaa atattcttta cccaccttaa tacgaaaana aatnnttatn cnccncnatg 180
qqtqqqqntn aaatcctnqc cccnttnccc tqttcnttta qqqaaccccc naattccccn 240
ngttattcct ctgtttgaaa nttctggttn cccggccctn tnaccaanag cttgannncc 300
nececqteet ggggeateet entgtttatt tteeetenan enececettn actn
<210> 32
<211> 477
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> misc feature
<222> (1)...(477)
<223> n = A, T, C or G
<400> 32
qqatcttttt qtqttttaca tqqttttata qqaaatactt caaqtttacc tqqtcqqqqt 60
tcactatggt attgaagtac ttcttctttt gtnactaaag ccataaccgc tcctttaagt 120
tgttctcaaa aagaatatag tcttatatgt attaatctat ttactattgt atagatacaa 180
taggtcataa aaaatattct attattattc tactgttatt atatagaata taaatgtgtt 240
atggctattg taactcacaa tatgttgtat aaagcatgta tggttaaata cctaaattat 300
tgtnccagca tcaacaaaaa naattcaccg gttactcctg atganaggtc tgaagctaaa 360
aaaacaqcaq atttacctac atcttccata nttacattac gttttaatgg tgaatgttct 420
cctatataat taaaaatttt tttgaagtcc aaatacnaaa gncgctaatg ttttata
<210> 33
<211> 568
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> misc feature
<222> (1)...(568)
<223> n = A, T, C or G
<400> 33
gatcatttaa aaaaccatct tgagtaaaac gaaaattccc tgctcgtgta tagtgtactt 60
tatcctctaa tgtaacctga aaaaaacctt ttccaccaat agcaagatct gttacactat 120
tgccaggttc aaaagcaccc tgtgtaaaaa ttgtgcgaac acttccaacc tgtgctccca 180
taccagootg gtttggcooc tgacttocag taaaacotat tgctaaatot tgactaaaca 240
ggtcttgaaa cactacctgt tgctgcttat acccaatggt atttgcgtta gcaatattat 300
tggagacagt accancectg tnetatgggt ttteatacet gttggcanea ataaacaaac 360
tccccatcat gataacatct cctaaaaaat aatttcatgg nggnaaaaat gttacctaca 420
catctctatt ttnaaagcaa aaaacccatg cccaanaaaa tttttgggcc naattaatat 480
acttaatcta ataaactttt ttgggtaatn aaaaaaaatt aattttttaa acttggtttn 540
                                                                   568
accaaccttt tctccttact ttttaacc
<210> 34
<211> 477
<212> DNA
<213> Lawsonia intracellularis
<220>
<221> misc feature
<222> (1)...(477)
<223> n = A, T, C or G
```

<400> 34						
ggtaccccac	ccgggtggaa	aatcgatggg	cccgcggccg	ctctaaaant	actctcgaga	60
agctttttga	attctttgga	tccccaggaa	taacttgttg	acggaatttt	acattttcta	120
tccctgcaaa	tanaaaaact	ttaccttgta	gttcattaat	aggaaaagat	tggagtactg	180
tgattccacc	tgattgcgcc	atagcttcta	aaattagaac	tccaggcatg	acaggaaatc	240
caggggaaat	gacccngaaa	aaatggttca	ttaatactaa	catttttata	agctttaata	300
tatttgccag	cattaaattc	aataactcta	tctacaatta	aaaagggata	acggtgggga	360
atttactgta	aaatttcttg	gatattttgg	aggtatggat	ggggacatta	attttcctat	420
atatatgctc	tttttcttt	cnaaaatttt	tcagcttttt	tatcccntaa	aaacctc	477